

592537 - 022402

BsiHKAI

TGTGCTCAAAGCCCCATTCAAAATGCCATTTAACGCATTGATACCTTCAGAAGAAAAA
1-----+-----+-----+-----+-----+-----+-----+-----+ 60
ACACGAGATTCGGGGTAAGTTTACGGTAAATTGCGTAACATGGAAAGTTCTTTT

a C A L K P P F K M P F N A F D T F K E K -

SmaI XmaI BsmI

ATTTTGAAACCCGGGAAGGAAGGAGTGAAGAATGCCGTAGGAGATCGCTGGGATCTTA
61-----+-----+-----+-----+-----+-----+-----+-----+ 120
TAAAACTTGGGCCCTCCTCCTACCTTACGGCATCCTCTAAGCGACCCCTAGAAT

a I L K P G K E G V K N A V G D S L G I L -

TaqI

CAAAGAAAATCGATGGGACCAACGAGGAGGGAGATGCCATTGAGCTGAGTGAGGAAGGA
121-----+-----+-----+-----+-----+-----+-----+-----+ 180
GTTTCTTTGAGCTACCTGGTGTGCTCCCTACGGTAACTCGACTCACTCCTCCT

a Q R K L D G T N E E G D A I E L S E E G -

StuI BsgI AlwNI

AGGCCTGTGCAGACATCCAGAGCCCAGGCCCTGTGTGCGACTGCAGCTGCTGTGGCATC
181-----+-----+-----+-----+-----+-----+-----+-----+ 240
TCCGGACACGTCTGTAGGTCTGGGCTGGGACACACGCTGACGTCGACGACACCGTAG

a R P V Q T S R A R A P V C D C S C C G I -

BspHI

CCCAAGCGGTACATCATCGCTGTCATGAGTGGCCTGGGATTCTGCATTTCTTGGGATT
241-----+-----+-----+-----+-----+-----+-----+-----+ 300
GGGTTGCCATGTAGTAGCGACAGTACTCACCGGACCTAAGACGTAAAGGAAACCCTAA

a P K R Y I I A V M S G L G F C I S F G I -

MscI XcmI

CGGTGCAACCTGGAGTGGCCATTGTGGAAATGGTCAACAAATAGCACTGTGTATGTGGAT
301-----+-----+-----+-----+-----+-----+-----+-----+ 360
GCCACGTTGGAACCTCACCGGTAACACCTTACCAAGTTACCGTTATCGTACACATACACCTA

a R C N L G V A I V E M V N N S T V Y V D -

Fig. 1

DRAFT

BsaWI | BsmBI
 361 GGGAAACCGGAAATCCAGACAGCACAGTTAACCTGGATCCAGAGACGGTGGGAAGGGCG
 CCCTTGGCCTTAGGTCTGCGTCAAATTGACCCTAGGTCTCTGCCACCCCTCCCGC 420

a G K P E I Q T A Q F N W D P E T V G R A -

NcoI | MaeIII
 421 AATTCTCTTATCCATGGATCTTTCTGGGTTATATTGTGACACAAATTCCCGGTGGC
 TTAAGAGAATAGGTACCTAGAAAAAGACCCAATATAACACTGTGTTAAGGCCACCG 480

a N S L I H G S F F W G Y I V T Q I P G G -

BsaHI | AatII
 481 TTCATTTCAAACAAGTTGCTGCTAACAGGGCTTGGAGCTGCCATCTCTTGACGTCA
 AAGTAAAGTTGTTCAAACGACGATTGTCAGAACCTCGACGGTAGAAGAACTGCAGT 540

a F I S N K F A A N R V F G A A I F L T S -

XmnI | SacII
 541 ACCCTGAACATGTTCATCCCTTCCGGCCAGGGTGCATTACGGCTGTGTCATGTGTG
 TGGGACTTGTACAAGTAGGAAAGGCAGCGCCGCCCCACGTAATGCCGACACAGTACACAC 600

a T L N M F I P S A A R V H Y G C V M C V -

AlwNI | MaeIII
 601 AGGATTTGCAGGGCTGGTGGAGGGTGTGACCTACCCAGCCTGCCACGGATGTGGAGT
 TCCTAAAACGTCCCAGACCACCTCCACACTGGATGGTCGGACGGTGCCTACACCTCA 660

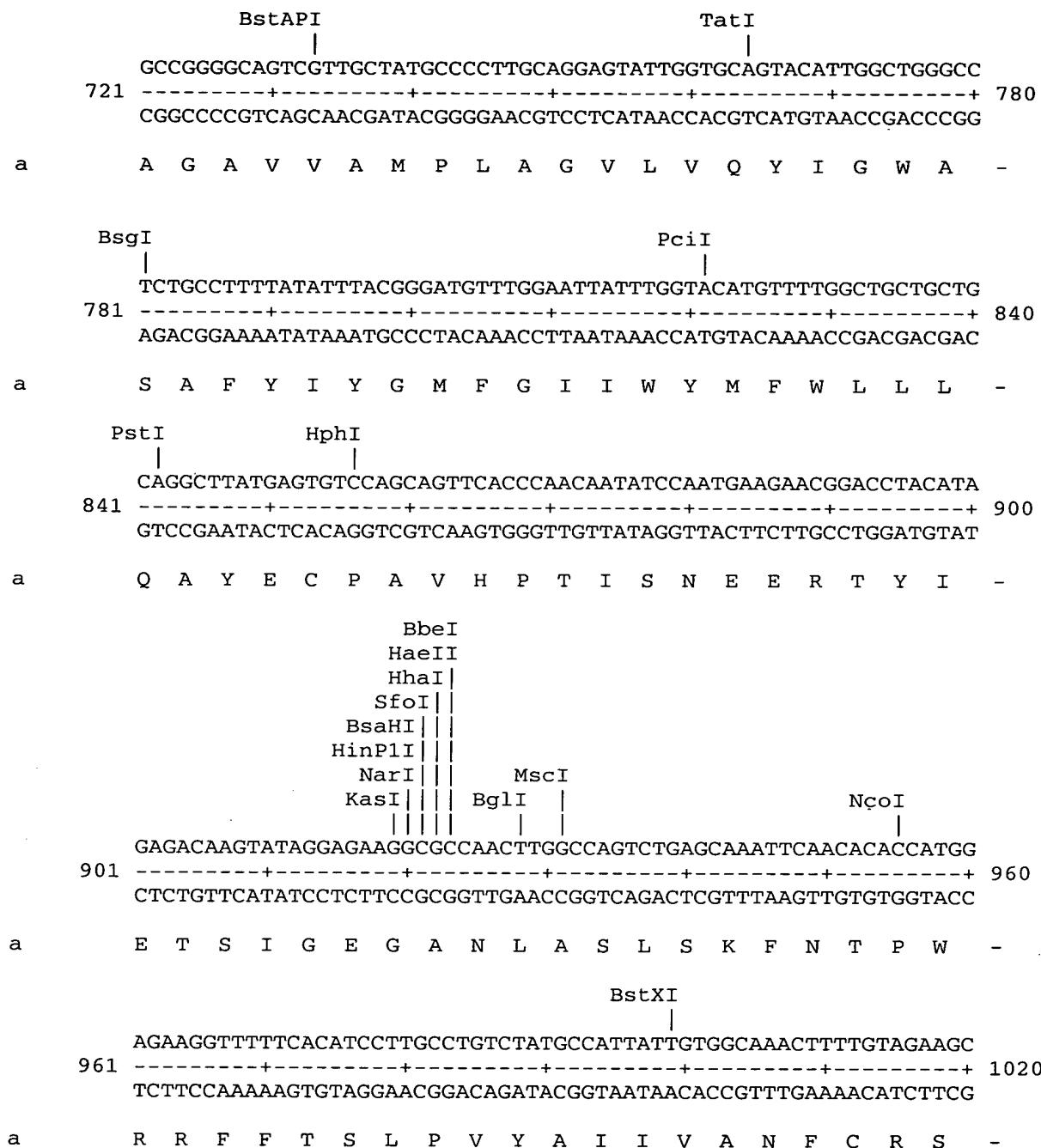
a R I L Q G L V E G V T Y P A C H G M W S -

BpmI |
 661 AAGTGGGCACCTCCCTGGAGAGAGAAGTCGTCTAGCCACAACCTCTTTGTGGTCCTAT
 TTCACCCGTGGAGGGACCTCTTCAGCAGATCGGTGTTGGAGAAAAACACCAAGGATA 720

a K W A P P L E R S R L A T T S F C G S Y -

Fig. 1 cont'd

0502151611 - 032250

***Fig. 1 cont'd***

DRAFT

TGGACCTCTATTGCTCTAATAAGTCAGCCTGCTTACTTGAAAGAGGTCTTGGTTT
 1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
 ACCTGGAAAGATAAACGAGAATTATCGTCGGACGAATGAAACTCTCCAGAAACCCAAA

a W T F Y L L I S Q P A Y F E E V F G F -
 BsAI PvuII DraIII BsaBI HphI Acc65I
 GCAATAAGTAAGGTGGGTCTCTTGTCAAGCTGTCCCACACATGGTGATGACAATCGTGGTA
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140
 CGTTATTCAATTCCACCCAGAGAACAGTCGACAGGGTGTGTACCACTACTGTTAGCACCAT

a A I S K V G L L S A V P H M V M T I V V -
 KpnI
 |
 CCCATTGGAGGACAACGGCTGATTATTAAGAACGCCGAAAGATTTGACCACAACTGCT
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200
 GGGTAACCTCCTGTTGACCGACTAATAATTCTCGGCTTCTAAAACGGTGTGACGA

a P I G G Q L A D Y L R S R K I L T T T A -
 BspHI
 |
 GTCAGAAAGATCATGAATTGGCTGATTATTAAGAACGCCGAAAGATTTGACCACAACTGCT
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260
 CAGTCTTCTAGTACTAACACCTCCGAAACCGTACCTCCGTGGAACGGGACACCAA

a V R K I M N C G G F G M E A T L L L V V -
 BstXI
 |
 GGGTTTCCATACCAAAGGAGTGGCTATCTCCTCCTGGTGTGCTGTAGGATTAGT
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320
 CCCAAAAGGGTATGGTTCCCTACCGATAGAGGAAGGACCACGACATCCTAAATCA

a G F S H T K G V A I S F L V L A V G F S -
 GGCTTGCAATTCAAGGTTCAATGTCAACCACCTGGACATTGCTCCACGATATGCCAGC
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380
 CCGAAACGTTAAAGTCCAAAGTTACAGTTGGTGGACCTGTAACGAGGTGCTATACGGTCG

a G F A I S G F N V N H L D I A P R Y A S -
 XcmI
 |
 ATCCTCATGGGATCTCAAATGGCGTGGGAACCCCTCTGGAAATGGTTGTCCCCCTCATT
 1381 -----+-----+-----+-----+-----+-----+-----+ 1440
 TAGGAGTACCCCTAGAGTTACCGCACCCCTGGGAGAGACCTTACCAAACAGGGGAGTAA

a I L M G I S N G V G T L S G M V C P L I -

Fig. 1 cont'd

SmaI | XbaI | XmnI
 GTTGGTGCAATGACAAAGCACAGACCCGGGAAGAATGGCAGAATGTGTTCCCTCATAGCA
 1441 CAACCACGTTACTGTTCGTGTCTGGGCCCTTACCGTCTTACACAAGGAGTATCGT
 V G A M T K H K T R E E W Q N V F L I A -
 BsiHKAI | MlyI
 ApaLI | PleI
 | |
 GCCCTGGTGCACTACAGTGGAGTCATCTCTACGGGTCTTGCTCTGGGAAAAACAG
 1501 CGGGACCACTGTGATGTCACCTCAGTAGAAGATGCCAGAACGAAGACCCCTTTGTC
 A L V H Y S G V I F Y G V F A S G E K Q -
 BmrI | BplI
 | |
 GACTGGGCTGATCCAGAGAATCTCTCTGAGGAGAAATGTGGAATCATTGACCAAGATGAA
 1561 CTGACCCGACTAGGTCTCTTAGAGAGACTCCTCTTACACCTTAGTAACTGGTTCTACTT
 D W A D P E N L S E E K C G I I D Q D E -
 BssSI
 |
 TTAGCCGAGGAAACAGAACTCAACCACGAGGCTTCGTAAGTCCCAGAAAGAAGATGTCT
 1621 AATCGGCTCCTTGCTCTGAGTTGGTGCCTCGAAAGCATTAGGGCTTCTACAGA
 L A E E T E L N H E A F V S P R K K M S -
 BbsI | EciI
 | |
 TATGGAGCCACCACCCAGAATTGTGAGGTCCAGAAGACGGATCGGAGACAAACAGAGAGAA
 1681 ATACCTCGGTGGTGGTCTAACACTCCAGGTCTCTGCCTAGCCTGTGCTCTCTT
 Y G A T T Q N C E V Q K T D R R Q Q R E -
 TaqI
 |
 TCCGCCTCGAGGGGGAGGAGCCATTATCCTACCAAGAATGAAGAGGACTTTCAGAAACA
 1741 AGGCAGGAAGCTCCCCCTCCTCGTAATAGGATGGTCTACTCTCCTGAAAAGTCTTGT
 S A F E G E E P L S Y Q N E E D F S E T -

Fig. 1 cont'd

BbvCI
Bpu10I

TCTTAACGTGCATCTCCCCCTCAGCTTACAACCAGAAGTCTCCACACCCATTGCTTTCC
1801 -----+-----+-----+-----+-----+-----+-----+-----+ 1860
AGAATTGCACGTAGAAGGGGAGTCGAATGTTGGTCTTCAGAGGTGTGGTAACGAAAAGG

a S * R A S S P Q L T T R S L H T H C F S -

Pf1MI

CATAACCTGGCCTTCCAGGGGGCAAATCACAGGAAAGGGGGAGACTAAATCAACAAACAG
1861 -----+-----+-----+-----+-----+-----+-----+ 1920
GTATGGAACCGGAAGGTCCCCCGGTTAGTGTCTTCCCCCTCTGATTAGTTGTC

a H T L A F Q G A K S Q E R G R L N Q Q Q -

BsaI

AGAAGAAAAATGCCTTCTTACAAAGATGGCGTATGGATCTGGTCTCAGTTAATTAGAT
1921 -----+-----+-----+-----+-----+-----+-----+ 1980
TCTTCTTTTACGGAAGAATGTTCTACCCGCATACCTAGAACCGAGACTCAATTATCA

a R R K M P S Y K D G R M D L G L S * L D -

BcI I MfeI

AGTTGATCATATTTTTGGGGGGGGCAATTGGGCATTGGCTGTTGAGCCTCTCTCAA
1981 -----+-----+-----+-----+-----+-----+-----+ 2040
TCAACTAGTATAAAAAAAACCCCCCCCCTAACCGTAACCGACAACCGAGAGAGTT

a S * S Y F F W G G Q L G I G C * A F S Q -

AAGAACAAATTATTTCAGGAAGAAATGGCTAGAAGAATAAGGAGTGGCTTGGCTCAAAT
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
TTCTTGTTAAATAAGTCCTCTTACCGATCTTCTTACCGATCTTCTTACCGAACACGAGTTA

a K N N L F R K K W L E E * G V A C C S N -

Eco57I TatI BpmI

AAACACTGAAGAAATCCCTTTGGTCTGGAGAAGAGTACATGGTGGTTGCCACCCATC
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
TTTGTGACTTCTTAGGGAGAAACCAGACCTCTCATGTACCACCAACGGTGGGTAG

a K H * R N P S L V W R R V H G G C H P I -

Fig. 1 cont'd

卷之三

	EcoRV	EcoNI	EcoO109I	PspOMI
2161	TCCAAGGATATCCATGTAGAGGACAATCTCTGCAACCTAATGAAGGGAAATCACTCATGGG AGGTTCCCTATAGGTACATCTCCTGTTAGAGACGTTGGATTACTTCCCTAGTGAGTACCC			
	S K D I H V E D N L C N L M K G I T H G -			
	ApaI			
co0109I	GGCCCTTGGTTGTGCCAGGTGCTTATGAACATTCTATTAACTCCCACACCCCTAACATAT CCGGGAACCAACACGGTCCACGAAATACTTGTAAGAATAATTGAGGGTGTGGGATTATA			
	G P W L C Q V L Y E H S Y L T P T P * Y -			
2281	AGTTATTGTACCCATTTACAACATAAGAACATTAAATGACTAGGTTGGCCCACCCAAGGT TCAATAACATGGTAAAATGTTGATTCTTGTAAATTACTGATCCAACCGGGTGGGTTCCA			
	S Y C T H F T T K N I K * L G W P T Q G -			
2341	TGT CCTCTCAGAGCAAAGCTGAGACTGGCAGATGACCAGGAGTTAGGAAGGAAGGAA ACAGGAGAGTCTCGGTTTCGACTCTGACCGTCTACTGGCCTCAAAATCCTCCTCCTT			
	C P L R A K A E T G R * P G V L G R K E -			
2401	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGGTTCAGTTGAGTGT CCTCCTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC			
	G R K E G R K E G R K E G R K G S V E C -			
2461	AGGGTCATTTCAATGACAAAAACAAAAACTGGAATCAGTTGGTTGTGGTAATTCCAT TCCCCAGTAAAGTTACTGTTTGTGACCTTAGTCACCAACAAACACCCATTAAGGTA			
	R V I F N D K N K N W N Q L V C G * F H -			
	SphI			
2521	GTTTGGTCAAGGGTGTGTCATGCAAACGTGTATGTGCGTGTGTGTGTTGTGTGTT CAAACCCAGTTCCCCACACACGTACGTTGCACATACACGCACACACACACACACACACAA			
	V W S R V C A C K R V C A C V C V C V F -			

Fig. 1 cont'd

2581 GNGTGTNAGNNNNATNANAANAAAAN
-----+-----+----- 2607
CNCACANTCNNNCNTANTNTNTTTTN

Fig. 1 cont'd

0 9 9 1 5 3 1 6 3 " 0 7 2 4 0 0 0 0

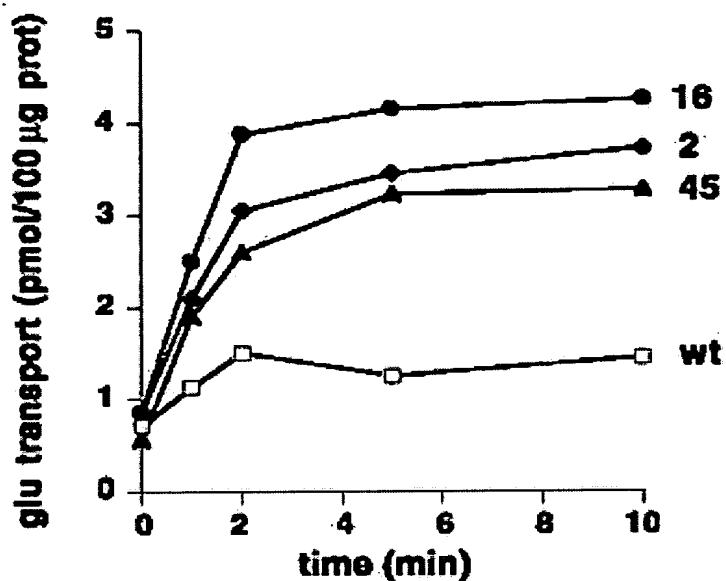


Fig. 2A

00015184-022403

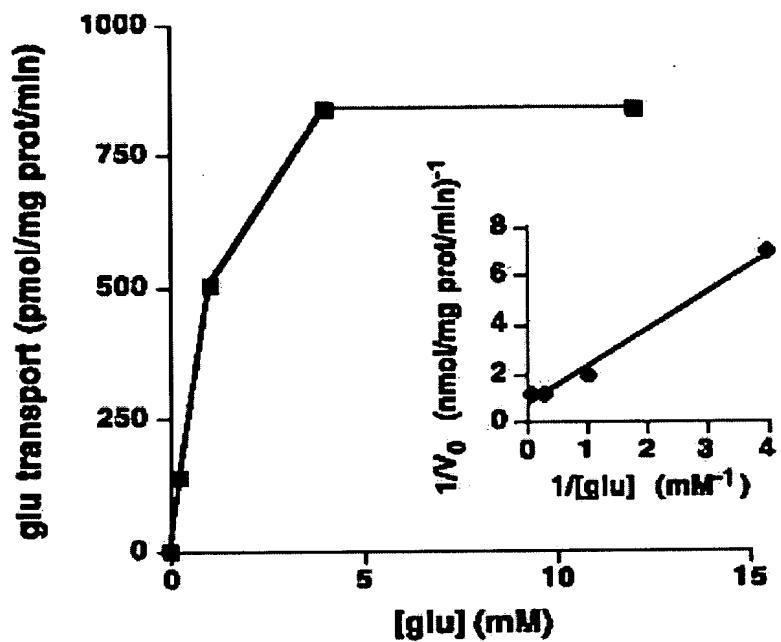


Fig. 2B

00953153837 3322403

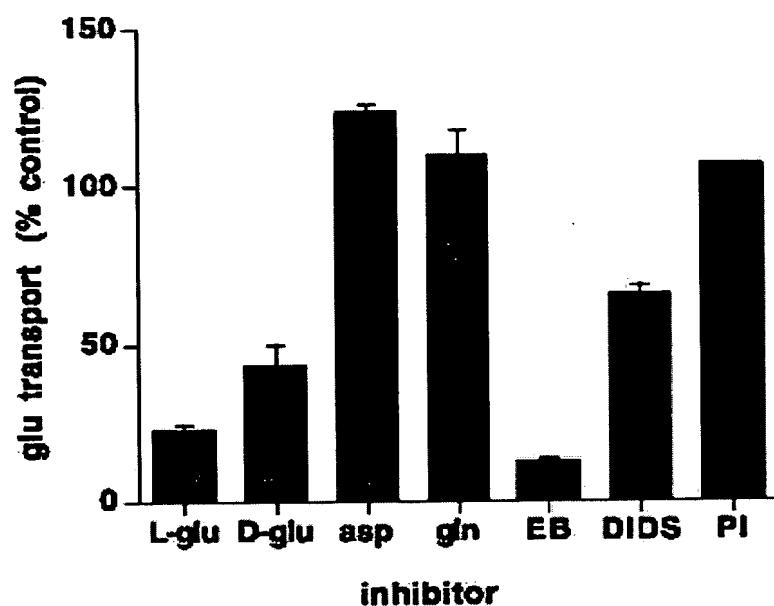


Fig. 3

09915181 - 072240

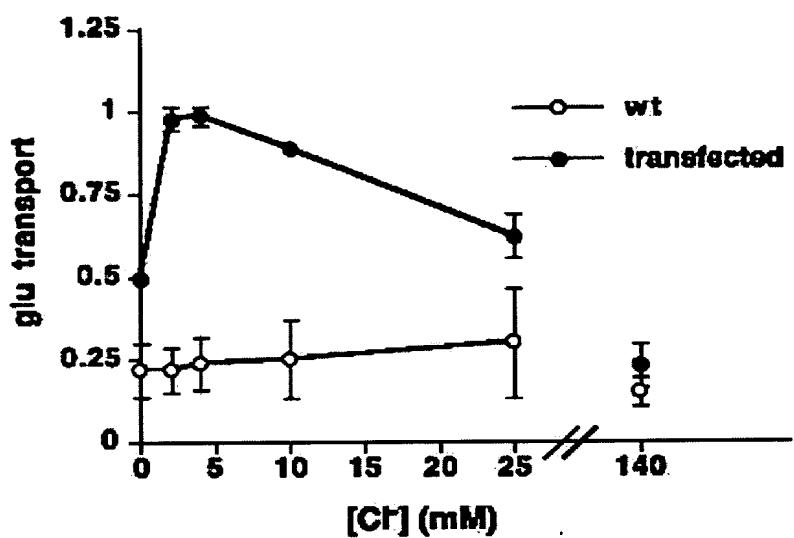


Fig. 4A

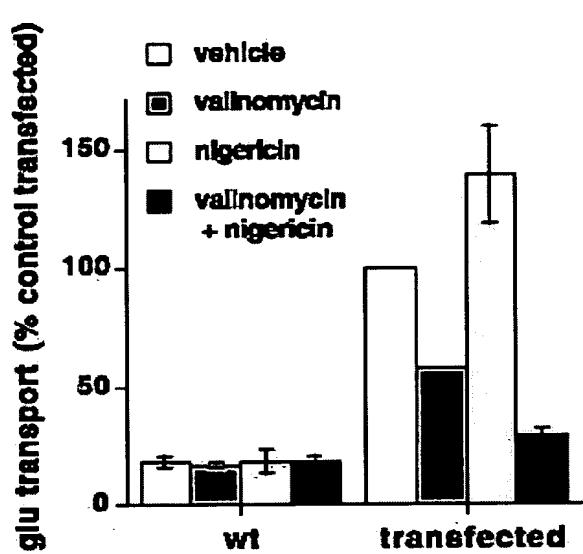


Fig. 4B



Fig. 5A

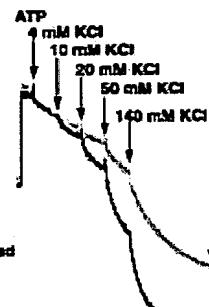


Fig. 5B

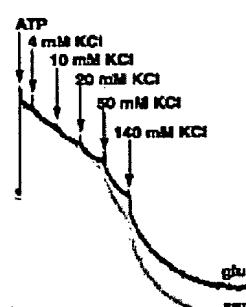


Fig. 5C

Fig. 5A, 5B, and 5C

1000 units
5 min

0024315431 "072400

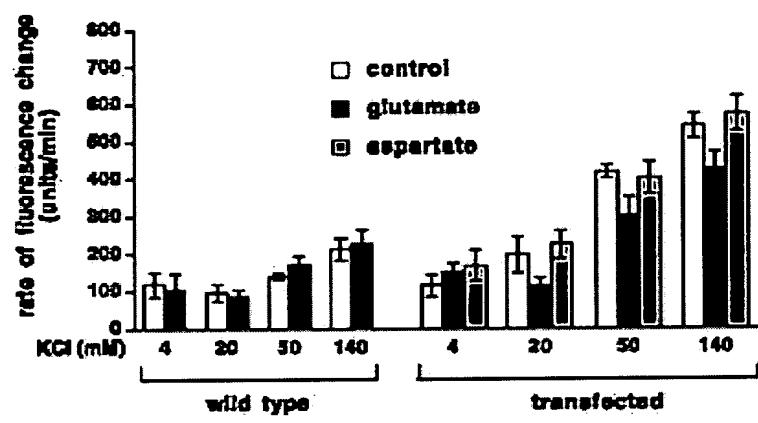


Fig. 5D

T00120 " T\$T\$T\$T\$0

MESVKQRILAPGKEGIKNNFAGKSLGQIYRVLKKQDNRETIELTE.DG..KPLEVPEKKA.PLCDCCTCF...GLPR.RYITIRAINSGLG 80
 MEFRQEERFKLLAGRLHRLKREGEATELELSA.DG..RPVTTHTRDP.PVVDCTCF...GLPR.RYICRIMSGLG 72
 EAT4 MVGEPLAKMTAAASATGAAPPQOMQE.EGNENPMMOMHSNKVLOVMEQTMI...GKCRKRWYALNLAANMG 66
 hsialin MRS PVRDLARNRDGEESTDRTPLLPAPRAEAAPV...CCCSARYNLAILAPPG 49
 rNaPi1 MENRCLPKKVPFGSFRYGLAILHFC 27

*
 rVGLUT2 FCISFGIRCNLGVAIDMVNNSTI...HRGCKVIKEKAK...FNWDPETVGWIHGSFFWGYINTQIPGGYIASRLAANRVP 155
 rVGLUT2 FCISFGIRCNLGVAIVSMVNNTD...HRGGHVUVVOKAQ...FNWDPETVGGLIHGSFFWGYIVTQIPGGFICORFAANRVP 147
 EAT4 FMIISFGIRCNLGAAKTHMVKNTD...PYGK...VHMHE...FNWTIDELSVMEES[FYGYEVTQIPPAQGELRAKEPPNKL 138
 hsialin FFIVYAAURVNLSVAVDMDVSNTLEDNRTSKACPEHSAP[KVHHNQTGKKYQWDAETOGWILGSFFYGYINTQIPGGYVASKIGKGKML 139
 rNaPi1 NIIVIMAQRVCNLNTMVAMVNKTTEPHHSNKSVAEMLDNVNRNPVH...SWSLDIQGLWLISSVFLGMWVIVQWPMVPGYLSGAYPMERKII 109

rVGLUT2 GAAIILSTLNMLIPSAARVHYG.CVIFVRILOGIVEGVTTYPACHGIWSKWAPPERSLATTAFCGSIYAGAVWAMPLAGVILQYTGWSS 244
 rVGLUT2 GFAIIVATSTLNMLIPSAARVHYG.CVIFVRILOGIVEGVTTYPACHGIWSKWAPPERSLATTAFTGSIYAGAVWAMPLAGVILQYTGWSS 236
 EAT4 GFGIGVGAFLNMLIPYCGKVKSDYLVAFQIOTLWFCUTPIAIDLGVPPLKAV.LRALEGEGVTEPAMHAWMSSWAPPLERSKLLSISYAGAQOLGTIVISPLSGITTCYMMNWY 228
 hsialin GFGIGLGTAVTLTFPIAIDLGVPPLKAV.LRALEGEGVTEPAMHAWMSSWAPPLERSKLLSISYAGAQOLGTIVISPLSGITTCYMMNWY 228
 rNaPi1 GSSEPLSSVLSLIPPAQQVG.AALVIVCRVQIQLQGQAOGAVSTGQHGIWVPMGPFIALLVUSGFVCDLLGWP 198

rVGLUT2 VFYVYGSFGMWYMFWLVSIESPAKHPTIDEERRVIEESISANLLGAMEKEKTPWRKEFTSMPPVXAIIVANFCRSWTFLYLISOP 334
 rVGLUT2 VFYVYGSFGFWYLFWLVSIESPAHPTISSEEERKVIEDAIIGHSHKQADWLRSNKILSTLCKVRFISLIGMICPAVFLVAAGEIGCDYISLAVAFLKTSSTTL 326
 EAT4 PTMKEALGMKIADEGKQHNSNKTPOKHKRISHYEKEYILSSLRQNQSSORSV.GROSPIKAMKSLPLWAIINWVAFIWSNNLVTYTP 316
 hsialin VFYVYGSFGFWLWLWVSDTPQKHKRISHYEKEYILSSLRQNQSSORSV.GROSPIKAMKSLPLWAIINWVAFIWSNNLVTYTP 313
 rNaPi1 VFYVYGSFGFWLWLWVSDTPQKHKRISHYEKEYILSSLRQNQSSORSV.GROSPIKAMKSLPLWAIINWVAFIWSNNLVTYTP 284

rVGLUT2 AYFEEVFGFEISKVGMLSAYPHLVMTIIVPIGGQIADFLRSKQILSTTIVRKIWNCGFGMEAATLLVVGYSHTR.GVAISFLVLAVGFS 423
 rVGLUT2 AYFEEVFGFEISKVGMLSAYPHLVMTIIVPIGGQIADFLRSKQILSTTIVRKIWNCGFGMEAATLLVVGYSHTR.GVAISFLVLAVGFS 415
 EAT4 PTMKEALGMKIADEGKQHNSNKTPOKHKRISHYEKEYILSSLRQNQSSORSV.GROSPIKAMKSLPLWAIINWVAFIWSNNLVTYTP 405
 hsialin VFYVYGSFGFWLWLWVSDTPQKHKRISHYEKEYILSSLRQNQSSORSV.GROSPIKAMKSLPLWAIINWVAFIWSNNLVTYTP 403
 rNaPi1 VFYVYGSFGFWLWLWVSDTPQKHKRISHYEKEYILSSLRQNQSSORSV.GROSPIKAMKSLPLWAIINWVAFIWSNNLVTYTP 374

rVGLUT2 GFAISGFGNVNHLIDIAPIRYASILMGISNGVGTLSGMVCPILIVGAMTKNSREWQYVFQESADPEETSE 513
 rVGLUT2 GFAISGFGNVNHLIDIAPIRYASILMGISNGVGTLSGMVCPILIVGAMTKNSREWQYVFQESADPEETSE 505
 EAT4 GFAISGFGNVNHLIDIAPIRYASILMGESNGCITLAGTCAAGTTCPPFAVTEAFTAH.SKRGWTSVFLASLIDQEWAEPEEMSE 494
 hsialin GFCSSGFGSNTNHLIDIAPIRYASAGILEGITPATTEPGMVGVCPVILKAVTALIGIFGETTSSTAGLILNQDPEYAWHKNFQGMAGINVTCLAFYLLFAKGDIODWAKETKETR 493
 rNaPi1 FSSFCGGQIANTALDIAPRYASILMGESNGCITLAGTCAAGTTCPPFAVTEAFTAH.SKRGWTSVFLASLIDQEWAEPEEMSE 464

rVGLUT2 EKCGFIIHDEDEL...DEETGDIQNYINIGTTSYGATSQENGWPNGWEKEEFPQESADAYSYKDRDDYS582 560
 rVGLUT2 EKCGFVGHDOLAGSDSESEMEDDEVPPGAPPAPPSSYGAT.HSTVQPPRPPVRDY 563
 EAT4 WSNRLEVNKTGINGTGYGAETTFQ..LPAGVDDSSYQAOAAPAGTNPFAASAWDEHGSSGVVENPHYQOW 495
 hsialin R H 465
 rNaPi1 L

Fig. 6A

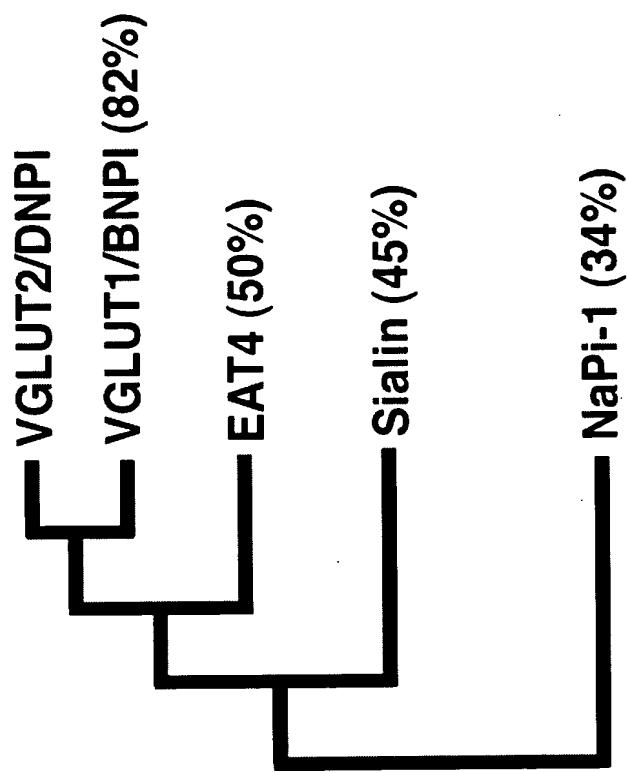


Fig. 6B

Fig. 7

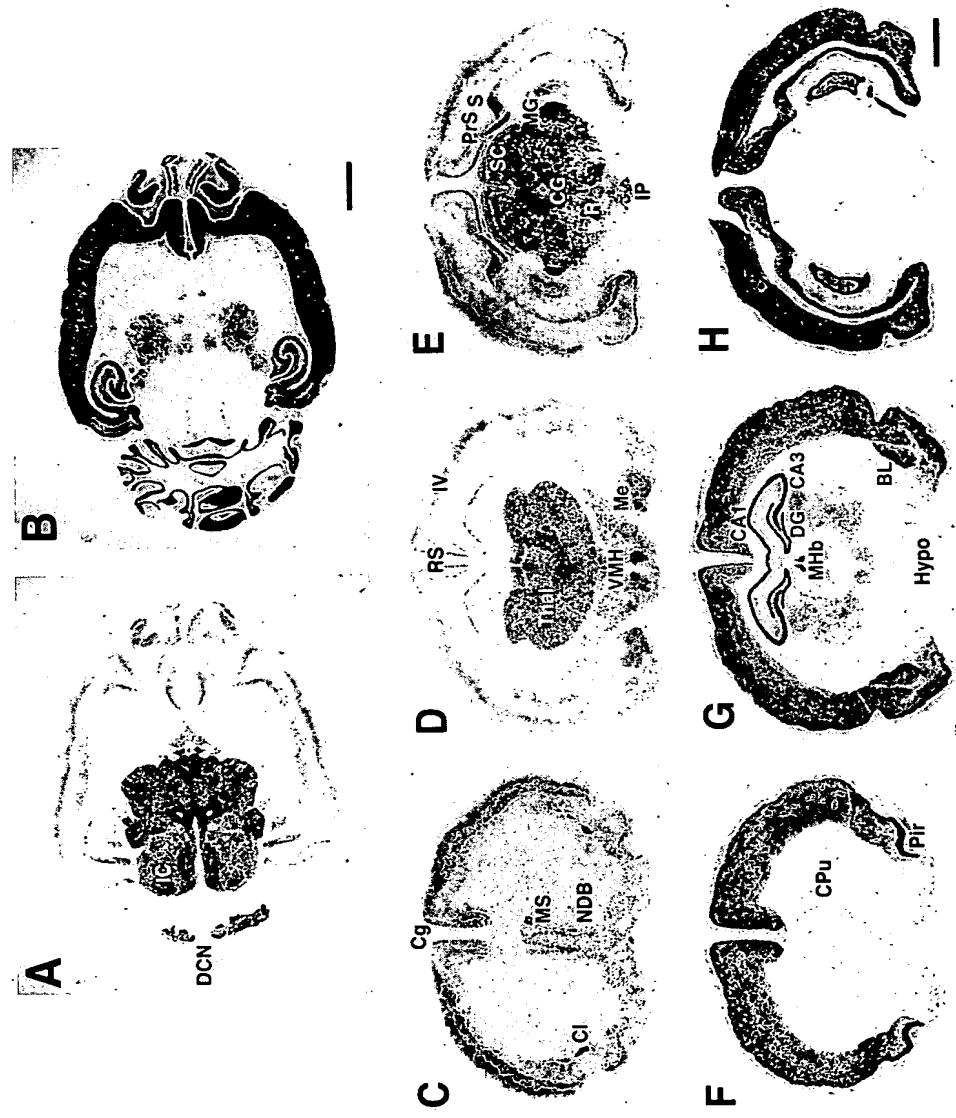
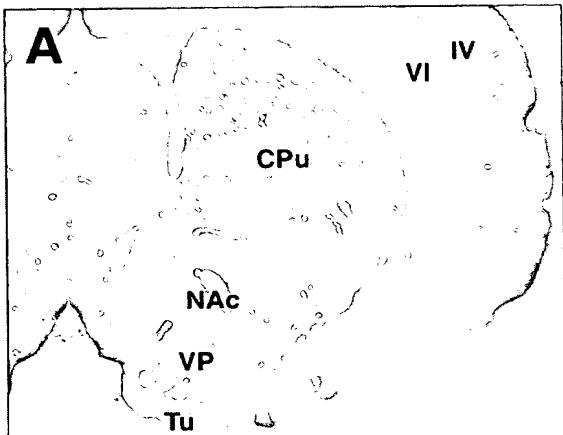


Fig. 7

09915181-022400

VGLUT2



VGLUT1

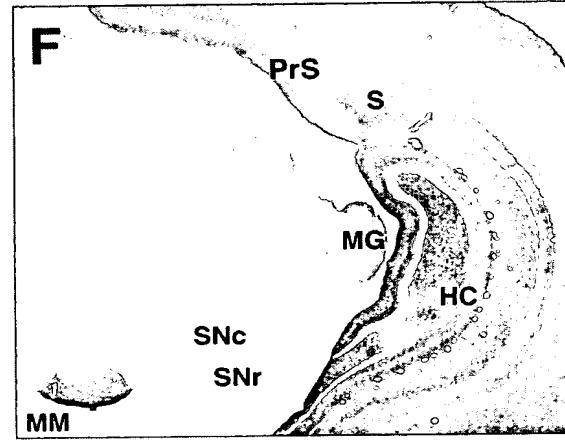
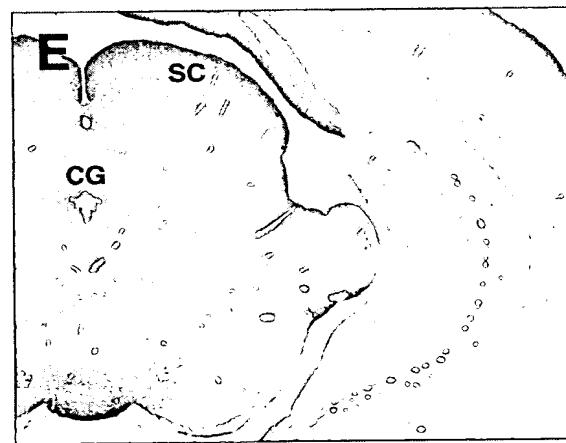
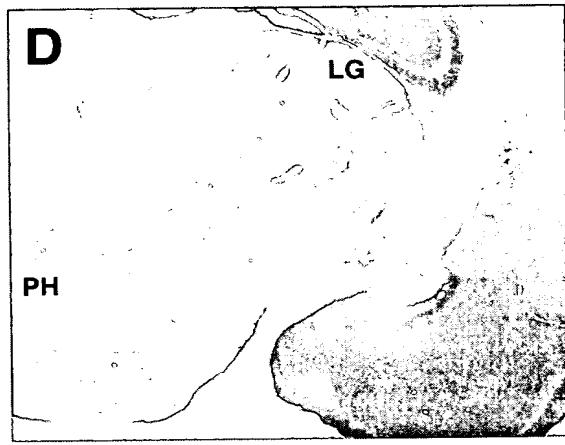
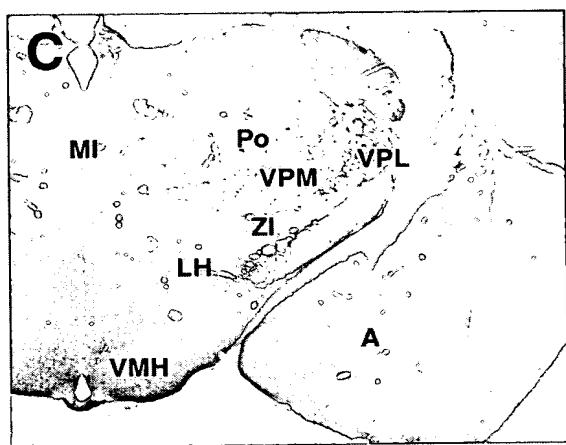
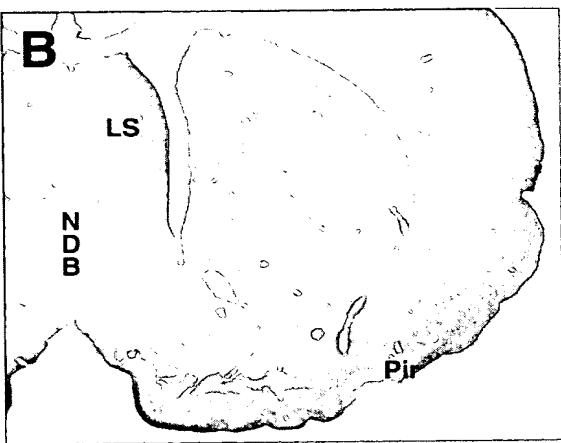


Fig. 8

09915181 • 002403

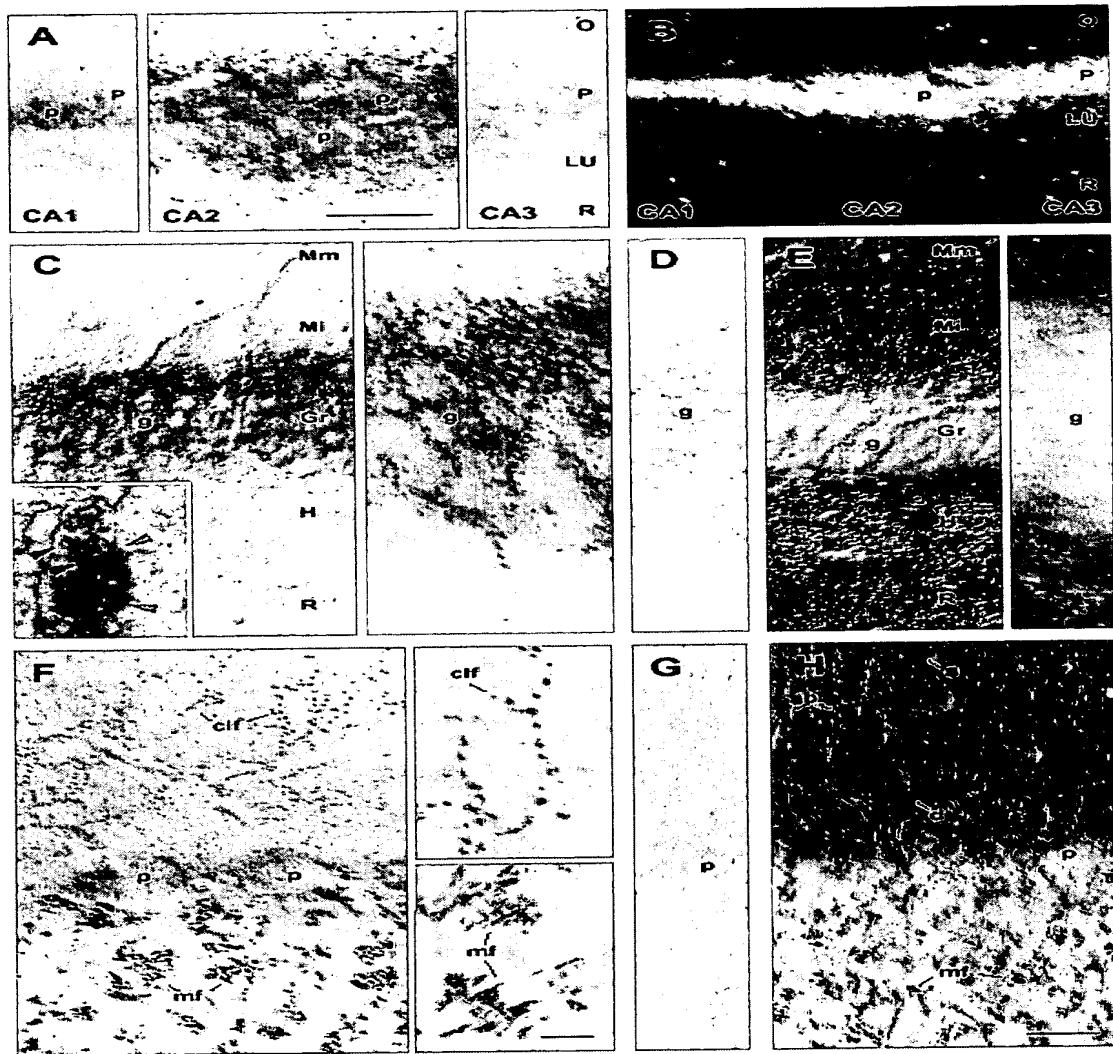


Fig. 9

Fig. 10A

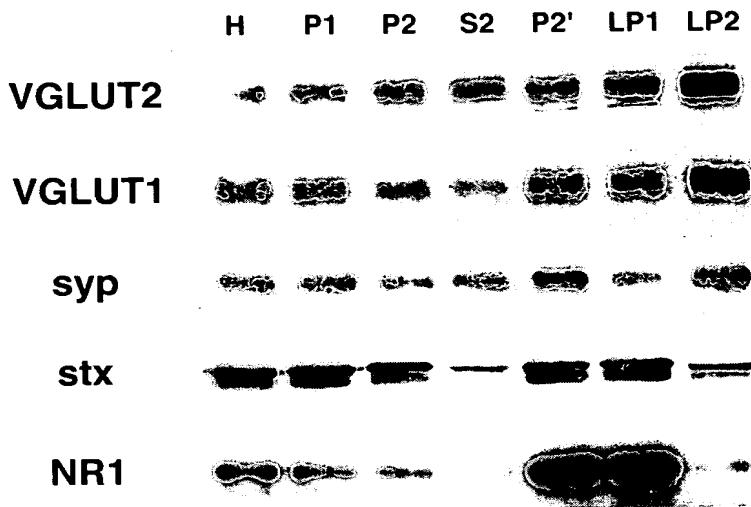


Fig. 10B

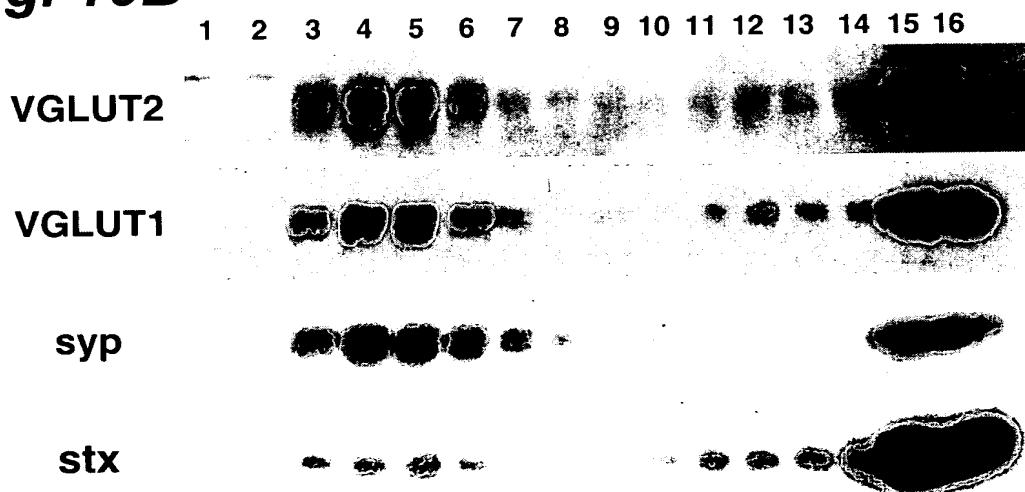


Fig. 11A

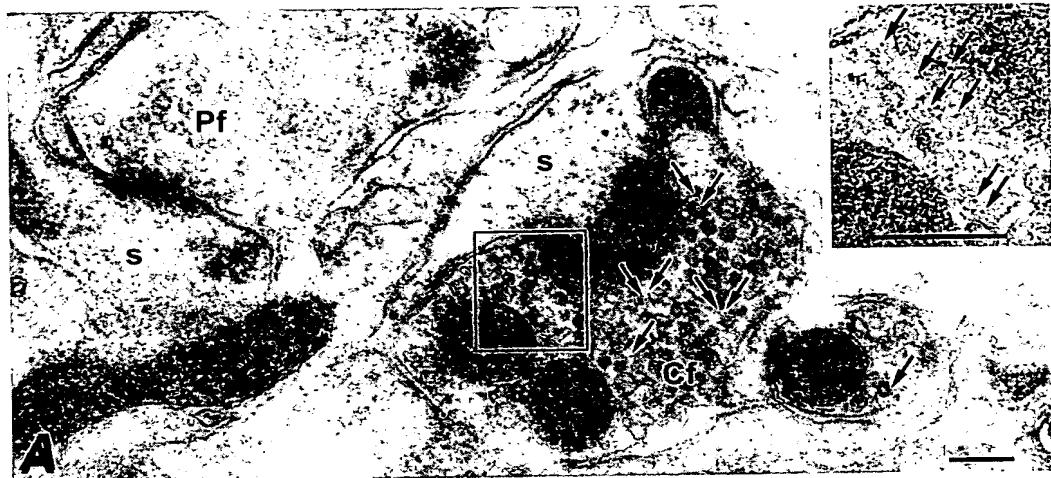


Fig. 11B

09315181 - 0722401

09915181 "072400

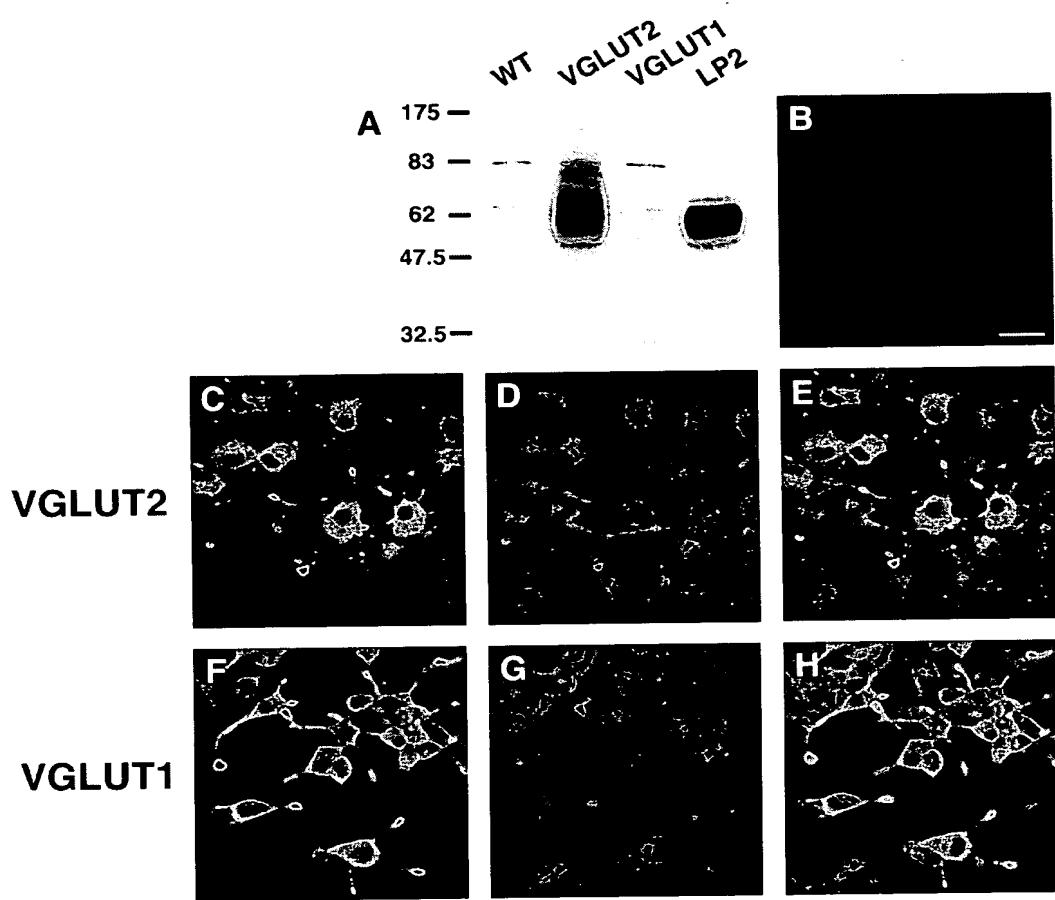


Fig. 12

Fig. 13A

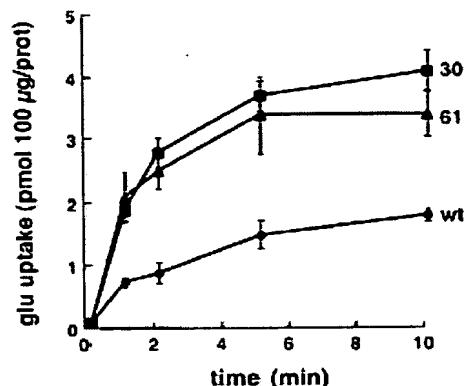


Fig. 13B

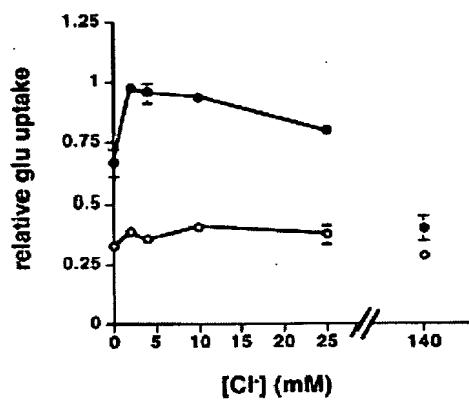
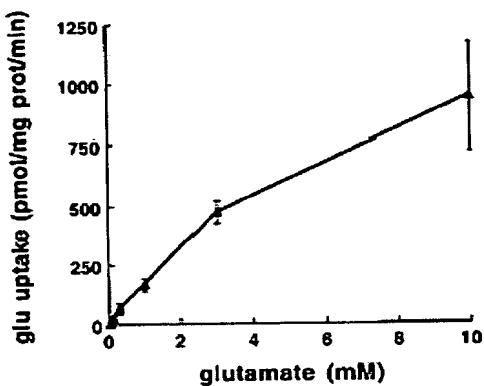


Fig. 13C

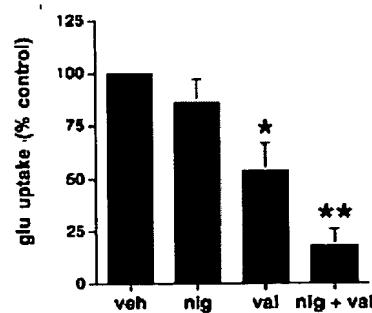


Fig. 13E